```
1    TCGGTCGCCTGAGAGGTATCACCTCTTCTGGGCTCAAGATGGACAACAAGAAGCGCCTGGCCTACGCCATCATCCAGTTCCTGCATGACCAGCTCCGGCA
                                  M  D  N  K  K  R  L  A  Y  A  I  I  Q  F  L  H  D  Q  L  R  H>

101  CGGGGGCCTCTCGTCCGATGCTCAGGAGAGCTTGGAAGTCGCCATCCAGTGCCTGGAGACTGCGTTTGGGGTGACGGTAGAAGACAGTGACCTTGCGCTC
     G  G  L  S  S  D  A  Q  E  S  L  E  V  A  I  Q  C  L  E  T  A  F  G  V  T  V  E  D  S  D  L  A  L >

201  CCTCAGACTCTGCCGGAGATATTTGAAGCGGCTGCCACGGGCAAGGAGATGCCGCAGGACCTGAGGAGCCCAGCGCGAACCCCGCCTTCCGAGGAGGACT
     P  Q  T  L  P  E  I  F  E  A  A  A  T  G  K  E  M  P  Q  D  L  R  S  P  A  R  T  P  P  S  E  E  D  S>

301  CAGCAGAGGCAGAGCGCCTCAAAACCGAAGGAAACGAGCAGATGAAAGTGGAAAACTTTGAAGCTGCCGTGCATTTCTACGGAAAAGCCATCGAGCTCAA
       A  E  A  E  R  L  K  T  E  G  N  E  Q  M  K  V  E  N  F  E  A  A  V  H  F  Y  G  K  A  I  E  L  N>

401  CCCAGCCAACGCCGTCTATTTCTGCAACAGAGCCGCAGCCTACAGCAAACTCGGCAACTACGCAGGCGCGGTGCAGGACTGTGAGCGGGCCATCTGCATT
     P  A  N  A  V  Y  F  C  N  R  A  A  A  Y  S  K  L  G  N  Y  A  G  A  V  Q  D  C  E  R  A  I  C  I >

501  GACCCGGCCTACAGCAAGGCCTACGGCAGGATGGGCCTGGCGCTCTCCAGCCTCAACAAGCACGTGGAGGCCGTGGCTTACTACAAGAAGGCGCTGGAGC
     D  P  A  Y  S  K  A  Y  G  R  M  G  L  A  L  S  S  L  N  K  H  V  E  A  V  A  Y  Y  K  K  A  L  E  L>

601  TGGACCCCGACAACGAGACATACAAGTCCAACCTCAAGATAGCGGAGCTGAAGCTGCGGGAGGCCCCCAGCCCCACGGGAGGCGTGGGCAGCTTCGACAT
       D  P  D  N  E  T  Y  K  S  N  L  K  I  A  E  L  K  L  R  E  A  P  S  P  T  G  G  V  G  S  F  D  I>

701  CGCCGGCCTGCTGAACAACCCTGGCTTCATGAGCATGGCTTCGAACCTAATGAACAATCCCCAGATTCAGCAGCTCATGTCCGGCATGATTTCGGGTGGC
       A  G  L  L  N  N  P  G  F  M  S  M  A  S  N  L  M  N  N  P  Q  I  Q  Q  L  M  S  G  M  I  S  G  G >

801  AACAACCCCTTGGGAACTCCCGGCACCAGCCCCTCGCAGAACGACCTGGCCAGCCTCATCCAGGCGGGCCAGCAGTTTGCCCAGCAGATGCAGCAGCAGA
     N  N  P  L  G  T  P  G  T  S  P  S  Q  N  D  L  A  S  L  I  Q  A  G  Q  Q  F  A  Q  Q  M  Q  Q  Q  N>
```

FIG. 1A

```
901   ACCCACAGTTGATAGAGCAGCTCAGGAGCCAATCCGGAGTCGGACGCCCAGCGCCAGCAACGACGACCAGCAGGAGTGACGCTGCCTGCTCCCGGTGTGA
       P  E  L  I  E  Q  L  R  S  Q  S  G  V  G  R  P  A  P  A  T  T  T  S  R  S  D  A  A  C  S  R  C  D>

1001  CCGCGTCCTTCCCTGGCCGACCCGAAGGAAGCCTTCTGGTTGTCTGCCACTTCCTCCTGTTGGACTGCCTGAGAGAGGGGAAGAGAGAGACCTCGGACCT
       R  V  L  P  W  P  T  R  R  K  P  S  G  C  L  P  L  P  P  V  G  L  P  E  R  G  E  E  R  D  L  G  P >

1101  GCATGTCAAGATGGATTTTCCCCTTTTATCTCTGCCCTCCTCCACTCCCTTTTTGTAACTCCCTTACAGCCCCCAGACCCTTCTTGAAACGAGAGCCAGC
      A  C  Q  D  G  F  S  P  F  I  S  A  L  L  H  S  L  F  V  T  P  L  Q  P  P  D  P  S  *

1201  AAGCTGAGCACAGACCAGCAGCGACCTCCCTTCCAGCCCCCAGAAAGCTCGGTCACTTGAGTGTTTTCTAGAATCCTGGGGTGCTCCCGGGCCGCTCTCA
1301  GAGAAGTGGCAGGTTTCACGTTCAGCCGTGTGGCGGATCGTGTGGCTTCCAAAGCCTTTTACAGCCCCCGCCCCCCATCCCGTGGTCTGTCTGCAGGAAC
1401  TCTCCCGTCTGTGAGAAGCCTCTTTCCGAGTCGACCTCCCGGCCACCCCGGCCCTGTGCCTGCTCGGAAGAGCTCACTGCCAGCTGCGGCCTGGGCACCG
1501  CGGGCCATGTGTGNTTGCATGAGGAACTCTTTAGTGGCAGACACCTAAGAGACGGCTGCGGTCACCCCACGCCTCCGTGGCTCAGGAGCCGTCCTGGGTG
1601  CATAGGACCAGTTTCTGTGACTTTTCTCCAGTTGGGCATGTTGACAGACATGTTTCCCCTCCTCCCACCCTCATTTTCTGGTCCTCGCGACTGAGAGCCA
1701  GGGGCGACATCATGACCTTCTGTCCCGGCCGCCTTAGCCCCGGGAACAGGGAAGGGAGCTGGGCCGTTTCTGTCTGTGTCCCATCCTGCTGTCCTTCTGT
1801  CCTGGATGTTTCATGGCCCGGGGCCCCCAGGGAAGCTTACCCCTCCTGTGCTGGGTGGAGGCCACGGGACACCTCAGGTGCCACCCACCTTGGCCCTA
1901  AAACAGCCACCAGGAAAGCAGCCGGAGAGCCGGACAGCGGGCAGCCTGTCTGGGTTCCTGAGGCCTGGGGGTGGCAGACGAACCCACGGCGCCGTGGTCC
2001  CAGCAGCAGGGTTGTCAGTCGGAGCATCCTGGGGCTCCCTGGCTCCTGGCCGTCTGTGAGGTAGGNGCAGTACCGTGTATCGTAGGTAGCAGTAGGAACG
2101  GGGGCCACCGCGGCCCTGCAGCCGTTCATGGCGGTGAGGTGTGTGCCAAGCCCACCCGGGGTGCAGGGCGTGACGTGTGGGGAATAAATAGGCGTTGTGA

2201  CCTCAAAAAAAAAAAAAAAAA
```

FIG. 1B

FIG. 2A

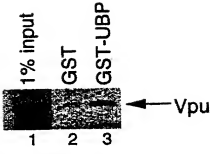

1% input
GST
GST-UBP
Vpu
1
2
3

FIG. 2B

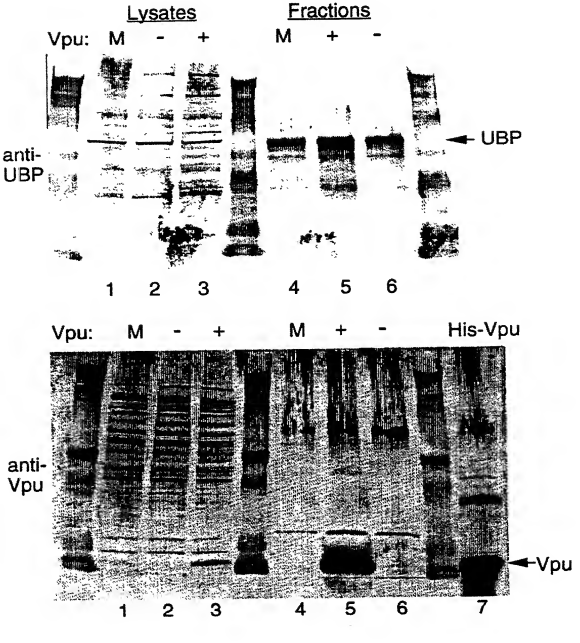

Lysates
Fractions
Vpu: M - + M + -
anti-UBP
UBP
1 2 3 4 5 6
Vpu: M - + M + - His-Vpu
anti-Vpu
Vpu
1 2 3 4 5 6 7

FIG 3A

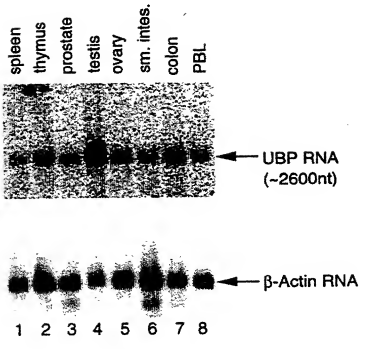
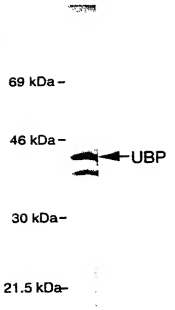


FIG 3B



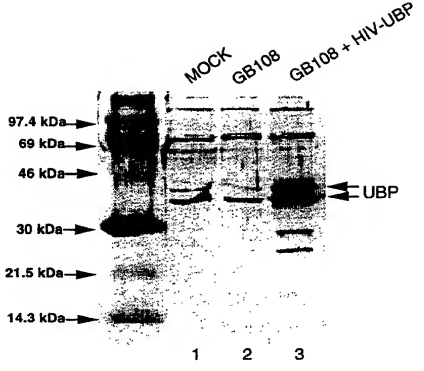


FIG 3C

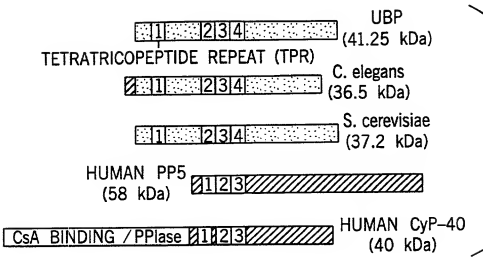


FIG. 4A

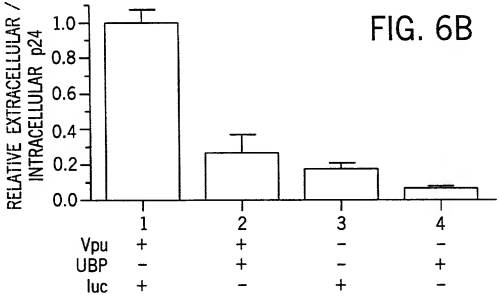


FIG. 6B

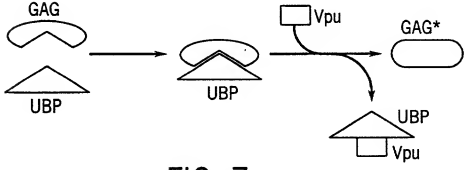
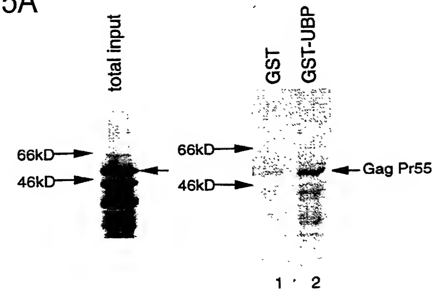


FIG. 7

FIG. 4B

```
CONSENSUS  * - - * G - * Y - - - - - * - - A * - - F - - A * - * - P - - - - -
                   A     F                       Y

UBP        L R H G G L S S D A Q E S L E V A I Q C L E T A F G V T V E D S D L  TPR1 (19-52)
C. eleg.   V S Q N Q A T A E Q A E A L E V A I Q C L E H S F G L D D A S Y A F  TPR1 (38-71)
S.cerev.   V E K K E I S E D G A D S L N V A M D C I S E A F G F E R E A V S G  TPR1 (20-53)

UBP        L K T E G N E Q M K V E N F E A A V H F Y G K A I E L N P A N A V Y  TPR2 (94-127)
C. eleg.   L K E E G N D L M K A S Q F E A A V Q K Y N A A I K L N R D P . V Y  TPR2 (108-140)
S.cerev.   L K M Q G N K A M A N K D Y E L A I N K Y T E A I K V L P T N A I Y  TPR2 (105-138)
PP5        L K T Q A N D Y F K A K D Y E N A I K F Y S Q A I E L N P S N A I Y  TPR1 (25-58)
CyP-40     L K N I G N T F F K S Q N W E M A I K K Y A E V L R Y V D S S K A V  TPR1 (226-259)

UBP        F C N R A A A Y S K L G N Y A G A V Q D C E R A I C I D P A Y S K A  TPR3 (128-161)
C. eleg.   F C N R A A A Y C R L E Q Y D L A I Q D C R T A L A L D P S Y S K A  TPR3 (141-174)
S.cerev.   Y A N R A A A H S S L K E Y D Q A V K D A E S A I S I D P S Y F R G  TPR3 (139-172)
PP5        Y G N R S L A Y L R T E C Y G Y A L G D A T R A I E L D K K Y I K G  TPR2 (59-92)
CyP-40     V L N I G A C K L K M S N W Q G A I D S C L E A L E L D P S N T K A  TPR2 (276-309)

UBP        Y G R M G L A L S S L N K H V E A V A Y Y K K A L E L D P D N E T Y  TPR4 (162-195)
C. eleg.   W G R M G L A Y S C Q N R Y E H A A E A Y K K A L E L E P N Q E S Y  TPR4 (175-208)
S.cerev.   Y S R L G F A K Y A Q G K P E E A L E A Y K K V L D I E G D N A T E  TPR4 (173-206)
PP5        Y Y R R A A S N M A L G K F R A A L R D Y E T V V K V K P H D K D A  TPR3 (93-126)
CyP-40     L Y R R A Q G W Q G L K E Y D Q A L A D L K K A Q G I A P E D K A I  TPR3 (310-343)
```

FIG. 5A


total input
GST
GST-UBP
66kD
46kD
66kD
46kD
Gag Pr55
1
2

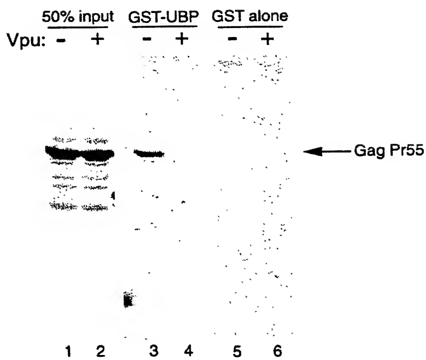

50% input
GST-UBP
GST alone
Vpu: - + - + - +
Gag Pr55
1 2 3 4 5 6

FIG. 5B

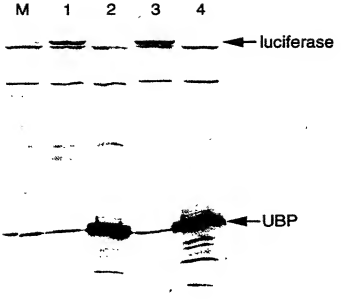


FIG. 6A